

AMENDMENTS TO THE SPECIFICATION

Please replace the previously submitted sequence listing with the replacement sequence listing submitted herewith.

Please replace the paragraph beginning at page 2, line 6, with the following rewritten paragraph:

A prokaryotic DNA repair ligase polypeptide may comprise an amino acid sequence from a prokaryotic cell which shares greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91), greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

Please replace the paragraphs beginning at page 2, line 18, with the following rewritten paragraphs:

A primase domain may share greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91) between residues 1-324, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

A nuclease domain may share greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91) between residues 325-447, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

A ligase domain may share greater than about 20% sequence identity with the sequence of Mt-Lig (CAB08492; SEQ ID NO: 91) between residues 448-759, greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

Please replace the paragraph beginning at page 3, line 15, with the following rewritten paragraph:

In some preferred embodiments, the prokaryotic DNA repair ligase polypeptide is an Mt-lig polypeptide. An Mt-lig polypeptide may comprise or consist of the amino acid sequence of database accession number CAB08492 (SEQ ID NO: 91), which is encoded by the M. tuberculosis ORF RV0938 (Z95209) or may be a variant or allele of this sequence.

Please replace the paragraph beginning at page 3, line 29, with the following rewritten paragraph:

A prokaryotic Ku polypeptide may comprise an amino acid sequence from a prokaryotic cell which shares greater than about 20% sequence identity with the sequence of Mt-Ku (CAB08491; SEQ ID NO: 92), greater than about 30%, greater than about 40%, greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 90% or greater than about 95% with the given amino acid sequence.

Please replace the paragraph beginning at page 4, line 5, with the following rewritten paragraph:

In preferred embodiments, the prokaryotic Ku polypeptide is an Mt-Ku polypeptide. An Mt-Ku polypeptide may comprise or consist of the amino acid sequence of database accession number CAB08491 (SEQ ID NO: 92) that is encoded by the M. tuberculosis ORF RV0937c (Z95209) or may be a variant or allele of this sequence.